



Fig. 1



Fig. 2 (Forts.)

432 T  
364 T T C A G A T A A C A G A A C A G G A T C A A C A A T T T T C C G A G C A A T T A C A T C T A T A A A G G  
208 A T G G A A T C T G C A T T C C C A G T C A C T G A G C A T C C T C A C C A T C C A G . . . C T C T G G G  
169 A T G G C A T C T G T A T T C C C A G T T A C T G A A G C A T C C T C A C C C G G . . . C T C T G G G  
449 A T G G A A T A T G C A T T C C C T C T G A C C A C A G C C A . . . T T T C C C G A 9 G G G A A T T G  
131 A T G G A A T A T G G G T C T G A T C A A A T C A . . . T T . . . C C G A G G A A A T T G  
166 A C G G A A T T G G T C C C A G A T C A A G A T G G A G C A A G A T G G A G C T T C C A A C C A A G G G A T A C C T G G G

Fig. 2 (Forts.)

433	616	AGAAAACAAAAGAAATCATGAGTGTATCATTGATGAAAGACTGTGAAACAGAAAGT	phdldk-3
424	617	GGAAACCCGGCATAGAGAAGCAGAACCACTGGTAACTGAAACCACTGGTAACTGAAAC	pcdkk-3
265	618	GGAAACCCGGCATAGAGAAGCAGAACCACTGGTAACTGAAACCACTGGTAACTGAAAC	pcdkk-2
226	619	GGAAACCCGGCATAGAGAAGCAGAACCACTGGTAACTGAAACCACTGGTAACTGAAAC	pcdkk-2
500	620	GGAAACCCGGCATAGAGAAGCAGAACCACTGGTAACTGAAACCACTGGTAACTGAAAC	phdldk-1
479	621	GGAAACCCGGCATAGAGAAGCAGAACCACTGGTAACTGAAACCACTGGTAACTGAAAC	phdldk-1
526	622	GGAAACCCGGCATAGAGAAGCAGAACCACTGGTAACTGAAACCACTGGTAACTGAAAC	phdldk-1
433	484	ATTGCCAGTTCCACCTTGGATA[AA]AG[GT]AGCCCTG[AA]AAACCC[AG]CATACAC[CT]	phdldk-3
325	485	GGATCTAGGAAGCCACACTCCAGA[AA]GGATGGCTCATAT[AA]AA[GG]AC[AT]GAGGAGACCC[AT]	pcdkk-3
206	486	GGATCTAGGAAGCCACACTCCAGA[AA]GGATGGCTCATAT[AA]AA[GG]AC[AT]GAGGAGACCC[AT]	pcdkk-2
560	487	GGATCTAGGAAGCCACACTCCAGA[AA]GGATGGCTCATAT[AA]AA[GG]AC[AT]GAGGAGACCC[AT]	phdldk-2
533	488	GGATCTAGGAAGCCACACTCCAGA[AA]GGATGGCTCATAT[AA]AA[GG]AC[AT]GAGGAGACCC[AT]	pcdkk-1
583	489	GGATCTAGGAAGCCACACTCCAGA[AA]GGATGGCTCATAT[AA]AA[GG]AC[AT]GAGGAGACCC[AT]	phdldk-1
433	544	GCTCACGGAGATGTTGAATGCTGGGA[GACCA]GCTTGTG[TT]G[GG]GAG[TC]GAG[TC]GAG[AA]G	phdldk-3
385	545	GCTTACGG[CA]CAGACTGCATTGAT[GG]TGTGCTGGC[CT]GGCAG[CT]GGCAG[AA]A	pcdkk-3
346	546	GCTTACGG[CA]CAGACTGCATTGAT[GG]TGTGCTGGC[CT]GGCAG[CT]GGCAG[AA]A	pcdkk-2
620	547	GCTTACGG[CA]CAGACTGCATTGAT[GG]TGTGCTGGC[CT]GGCAG[CT]GGCAG[AA]A	phdldk-2
593	548	GCTTACGG[CA]CAGACTGCATTGAT[GG]TGTGCTGGC[CT]GGCAG[CT]GGCAG[AA]A	pcdkk-1
643	549	GCTTACGG[CA]CAGACTGCATTGAT[GG]TGTGCTGGC[CT]GGCAG[CT]GGCAG[AA]A	phdldk-1

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453	AGCCACAGTACTACATCTGACTGACTGTTGAACTGTTCCAAATGAAACGGA[AAA
843	ATGATGGAAACCTGGATTGGAAATGCGGATGAGGGATG166TAAGAATG166AGCA6
670	ATGGTGGAAATTAGGTTAGATGGAGAAAT...66CTAAATAAGAAACG16A[AAAG
640	CTTATGATTGTCAGCTCAATCCCAGGATGTAAGGAATCTTCAGT61GTTAAAGCAT
910	029
941	CTGCACTGTTTACATGAACTGACTGTTGCTGCTGGTCCTGGAA[GGC16

Fig. 2 (Forts.)



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143	CATACACCTTAACAGATACTGGATAGAAGTAAACATCTTCACTGAGCATCC	phdak-3
882	.....	predk-3
769	.....	predk-2
1210	AAAAAAAGAAAAAAA.....	phdak-2
829	.....	predk-1
1241	TATTTTAAATTGAAATTAAAACATTTCATAACCTTAAACCAAAA.....	phdak-1
435	.....	predk-1
1203	GTTTTCGTCACAAATTCACTGATGTTCTGCACACCTGTTTCACTGAGACC	predk-3
882	.....	predk-2
769	.....	predk-2
1227	.....	predk-1
829	.....	predk-1
1298	.....	predk-1
433	.....	predk-3
1263	AAACTTTCATCAAGACAAATGAGAAAAGGCCATAGGATTAAATCCCTTC	predk-3
882	.....	predk-2
769	.....	predk-2
1257	.....	predk-1
829	.....	predk-1
1298	.....	predk-1

Fig. 2 (Forts.)

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Fig. 2 (Forts.)

11/11/2008  
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Fig. 3

